

10/539688

SEQUENCE LISTING

<110> Slamon, Dennis J.
Anderson, Lee A.
Ginther, Charles L.
The Regents of the University of California

<120> Amplified and Overexpressed Gene in Colorectal Cancers

<130> 023070-129910US

<140> US 10/539,868
<141> 2005-06-16

<150> US 10/346,367
<151> 2003-01-15

<150> WO PCT/US04/01153
<151> 2004-01-15

<160> 28

<170> PatentIn Ver. 2.1

<210> 1
<211> 1605
<212> DNA
<213> Homo sapiens

<220>
<223> 26#77 protein

<400> 1
ctttgggggt ttgctgctgg ctctgactcc cgtcctgcga tgggttgcca cgggggaaca 60
atccccaaga ggcataaact ggtgaagggg ccgaagaagg ttgagaaggt cgacaaagat 120
gctgaattag tggcccaatg gaactattgt actctaagtc aggaaatatt aagacgacca 180
atagttgcct gtgaacttgg cagactttat aacaaagatg ccgtcattga atttctcttg 240
gacaaatctg cagaaaaggc tcttggaag gcagcatctc acattaaaag cattaagaat 300
gtgacagagc tgaagctttc tgataatcct gcctgggaag gggataaagg aaacactaaa 360
ggtgacaagc acgatgacct ccagcgggag cgtttcatct gcccgttgt gggcctggag 420
atgaacggcc gacacagggt ctgcttcctt cgggtgctgc gctgtgtgtt ttctgagcga 480
gccttgaaag agataaaagc ggaagtttgc cacacgtgtg gggctgcctt ccaggaggat 540
gatgtcatcg tgctcaatgg caccaaggag gatgtggagc tgctgaagac aaggatggag 600
gagagaaggc tgagagcgaa gctggaaaag aaaacaaaga aaccaaggc agcagagtct 660
gtttcaaaac cagatgtcag tgaagaagcc ccaggggccat caaaagttaa gacagggag 720
cctgaagagg ccagccttga ttctagagag aagaaaacca acttggtctc caaaagcaca 780
gcaatgaatg agagctcttc tggaaaagct ggggaagcctc cgtgtggagc cacaagagg 840
tccatcgctg acagtgaaga atcgagggcc tacaagtccc tctttaccac tcacagctcc 900
gccaagcgct ccaaggagga gtctgcccac tgggtcacc acacgtccta ctgcttctga 960
agcccgact gccaccgctc ctgcccaga aggttggtta gtttccacgt aggcaggtcg 1020
ctttgtgcct ctgagtgcgc tgctgtgtgt tctctctata gttctgcgtc ataaagctgt 1080
cctggccagc cttcaagctg gtgtggccac tcttgatgtg aggcgtgtcg gttccagggg 1140
ggacatggga ggggctgcac agtggcccgga ggtcatgctt gcttccacct gcaggtgcat 1200
ttggtccttt ccatggccag gaagccctgt gggctgcact ttttatgctt gcagtagcaa 1260
gagactccag agtcctcacc ggtgcagagt tggcacatat taattaacta aaattctaata 1320
gatcttgcta ccagcaataa atcaagtagg ccaagtgaag ctgggcttta aaaaggatgg 1380
atttcaaata cactgtgccc actagaagct tcgaagggcc tcgtccctct gctacagccc 1440
tgggaggagc caggatcctt gttggtctag ctaataactg ttaggggagt gtgccccatc 1500
tcatcatttc gaagatagca gagtcatagt tgggcaccgc gtgattgggt tcaaaaataa 1560
agctggtctg cctcttctca aaaaaaaaaa aaagaaaaaa aaaaaa 1605

<210> 2
 <211> 306
 <212> PRT
 <213> Homo sapiens

<220>
 <223> 26#77 protein

<400> 2
 Met Gly Cys Asp Gly Gly Thr Ile Pro Lys Arg His Glu Leu Val Lys
 1 5 10 15
 Gly Pro Lys Lys Val Glu Lys Val Asp Lys Asp Ala Glu Leu Val Ala
 20 25 30
 Gln Trp Asn Tyr Cys Thr Leu Ser Gln Glu Ile Leu Arg Arg Pro Ile
 35 40 45
 Val Ala Cys Glu Leu Gly Arg Leu Tyr Asn Lys Asp Ala Val Ile Glu
 50 55 60
 Phe Leu Leu Asp Lys Ser Ala Glu Lys Ala Leu Gly Lys Ala Ala Ser
 65 70 75 80
 His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
 85 90 95
 Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
 100 105 110
 Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
 115 120 125
 Asn Gly Arg His Arg Phe Cys Phe Leu Arg Cys Cys Gly Cys Val Phe
 130 135 140
 Ser Glu Arg Ala Leu Lys Glu Ile Lys Ala Glu Val Cys His Thr Cys
 145 150 155 160
 Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Val Leu Asn Gly Thr Lys
 165 170 175
 Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
 180 185 190
 Ala Lys Leu Glu Lys Lys Thr Lys Lys Pro Lys Ala Ala Glu Ser Val
 195 200 205
 Ser Lys Pro Asp Val Ser Glu Glu Ala Pro Gly Pro Ser Lys Val Lys
 210 215 220
 Thr Gly Lys Pro Glu Glu Ala Ser Leu Asp Ser Arg Glu Lys Lys Thr
 225 230 235 240
 Asn Leu Ala Pro Lys Ser Thr Ala Met Asn Glu Ser Ser Ser Gly Lys
 245 250 255
 Ala Gly Lys Pro Pro Cys Gly Ala Thr Lys Arg Ser Ile Ala Asp Ser
 260 265 270

Glu Glu Ser Glu Ala Tyr Lys Ser Leu Phe Thr Thr His Ser Ser Ala
 275 280 285

Lys Arg Ser Lys Glu Glu Ser Ala His Trp Val Thr His Thr Ser Tyr
 290 295 300

Cys Phe
 305

<210> 3
 <211> 2211
 <212> DNA
 <213> Homo sapiens

<220>
 <223> copine 1 (CPNE 1, CPN1) protein

<400> 3
 ggcgaaggct ttgtagagtt cagaaatgag gctgactata aggctgctct gtgtcgtcat 60
 aaacagtaca tgggcaatcg ctttattcaa gttcatccaa ttactaagaa aggtatgcta 120
 gaaaagatag atatgattcg aaaaagactg cagaacttca gctatgacca gagggaaatg 180
 atactaaatc cagaggggga tgtcaactct gccaaagtct gtgcccacat aacaaatatt 240
 ccattcagca ttacaaagat ggatgttctt cagttcctag aaggaatccc agtggatgaa 300
 aatgctgtac atgttcttgt tgataacaat gggcaaggct taggacaggc attggttcag 360
 tttaaaaatg aagatgatgc acatggccca ctgcgtgacc ttgggtcagc tgtccatttc 420
 ctgtgaccat ctcattgaca aggacatcgg ctccaagtct gacccactct gcgtcctttt 480
 acaggatgtg ggagggggca gctgggctga gcttggccgg actgaacggg tgcggaactg 540
 ctcaagccct gagttctcca agactctaca gcttgagtac cgctttgaga cagtccagaa 600
 gctacgcttt ggaatctatg acatagacaa caagacgcca gagctgaggg atgatgactt 660
 cctagggggg cctgagtggt ccctaggaca gattgtgtcc agccaggtag tgactctccc 720
 cttgatgctg aagcctggaa aacctgctgg gcggggggacc atcacggtct cagctcagga 780
 attaaaggac aatcgtgtag taaccatgga ggtagaggcc agaaacctag ataagaagga 840
 cttcctggga aaatcagatc catttctgga gttcttccgc cagggtgatg ggaaatggca 900
 cctgggtgtac agatctgagg tcatcaagaa caacctgaac cctacatgga agcgtttctc 960
 agtccccgtt cagcatttct gtggtgggaa cccacgcaca cccatccagg tgcaatgctc 1020
 cgattatgac agtgacgggt cacatgatct catcggtagc ttccacacca gcttggccca 1080
 gctgcaggca gtcccggctg agtttgaatg catccaccct gagaagcagc agaaaaagaa 1140
 aagctacaag aactctggaa ctatccgtgt caagatttgt cgggtagaaa cagagtactc 1200
 ctttctggac tatgtgatgg gaggtgttca gatcaacttc actgtgggag tggacttcac 1260
 tggctccaat ggagaccctt cctcacctga ctccctacac tacctgagtc caacaggggt 1320
 caatgagtac ctgatggcac tgtggagtggt gggcagcgtg gttcaggact atgactcaga 1380
 caagctgttc cctgcatttg gatttggggc ccagggtccc cctgactggc aggtctcgca 1440
 tgaatttgcc ttgaatttca accccagtaa cccctactgt gcaggcatcc agggcattgt 1500
 ggatgcctac cgccaagccc tgccccaagt tcgcctctat ggccctacca actttgcacc 1560
 catcatcaac catgtggcca ggtttgcagc ccagggtgca catcagggga ctgcctcgca 1620
 atacttcatg ctgttgctgc tgactgatgg tgctgtgacg gatgtggaag ccacacgtga 1680
 ggctgtggtg cgtgcctcga acctgcccac gtcagtgatc attgtgggtg tgggtggtgc 1740
 tgacttttag gccatggagc agctggagcg tgatggtgga cccctgcata cacgttctgg 1800
 gcaggctgct gccgcgaca ttgtgcagtt tgtacctac cgccgggttc agaatgcccc 1860
 tcgggaggca ttggcacaga ccgtgctcgc agaagtgcc acacaactgg tctcatactt 1920
 cagggccag ggttggggcc cgctcaagcc acttccaccc tcagccaagg atcctgcaca 1980
 ggccccccag gcctaggttc ccttgagggc tgtggcaagt cctcaatcct gtgtcccaga 2040
 ggtccctctg ggccacaacc caacccttct cactctctct agtgctagca ctttgtattt 2100
 tttgatactt ttatacttgt ttctgctttt gctgctcttg atcccacctt tgctcctgac 2160
 aaccctcatt caataaagac cagtgaagac caaaaaaaaa aaaaaaaaaa a 2211

<210> 4
 <211> 537
 <212> PRT
 <213> Homo sapiens

<220>
 <223> copine 1 (CPNE 1, CPN1) protein

<400> 4
 Met Ala His Cys Val Thr Leu Val Gln Leu Ser Ile Ser Cys Asp His
 1 5 10 15
 Leu Ile Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val Leu
 20 25 30
 Leu Gln Asp Val Gly Gly Gly Ser Trp Ala Glu Leu Gly Arg Thr Glu
 35 40 45
 Arg Val Arg Asn Cys Ser Ser Pro Glu Phe Ser Lys Thr Leu Gln Leu
 50 55 60
 Glu Tyr Arg Phe Glu Thr Val Gln Lys Leu Arg Phe Gly Ile Tyr Asp
 65 70 75 80
 Ile Asp Asn Lys Thr Pro Glu Leu Arg Asp Asp Asp Phe Leu Gly Gly
 85 90 95
 Ala Glu Cys Ser Leu Gly Gln Ile Val Ser Ser Gln Val Leu Thr Leu
 100 105 110
 Pro Leu Met Leu Lys Pro Gly Lys Pro Ala Gly Arg Gly Thr Ile Thr
 115 120 125
 Val Ser Ala Gln Glu Leu Lys Asp Asn Arg Val Val Thr Met Glu Val
 130 135 140
 Glu Ala Arg Asn Leu Asp Lys Lys Asp Phe Leu Gly Lys Ser Asp Pro
 145 150 155 160
 Phe Leu Glu Phe Phe Arg Gln Gly Asp Gly Lys Trp His Leu Val Tyr
 165 170 175
 Arg Ser Glu Val Ile Lys Asn Asn Leu Asn Pro Thr Trp Lys Arg Phe
 180 185 190
 Ser Val Pro Val Gln His Phe Cys Gly Gly Asn Pro Ser Thr Pro Ile
 195 200 205
 Gln Val Gln Cys Ser Asp Tyr Asp Ser Asp Gly Ser His Asp Leu Ile
 210 215 220
 Gly Thr Phe His Thr Ser Leu Ala Gln Leu Gln Ala Val Pro Ala Glu
 225 230 235 240
 Phe Glu Cys Ile His Pro Glu Lys Gln Gln Lys Lys Lys Ser Tyr Lys
 245 250 255
 Asn Ser Gly Thr Ile Arg Val Lys Ile Cys Arg Val Glu Thr Glu Tyr
 260 265 270

Ser Phe Leu Asp Tyr Val Met Gly Gly Cys Gln Ile Asn Phe Thr Val
 275 280 285
 Gly Val Asp Phe Thr Gly Ser Asn Gly Asp Pro Ser Ser Pro Asp Ser
 290 295 300
 Leu His Tyr Leu Ser Pro Thr Gly Val Asn Glu Tyr Leu Met Ala Leu
 305 310 315 320
 Trp Ser Val Gly Ser Val Val Gln Asp Tyr Asp Ser Asp Lys Leu Phe
 325 330 335
 Pro Ala Phe Gly Phe Gly Ala Gln Val Pro Pro Asp Trp Gln Val Ser
 340 345 350
 His Glu Phe Ala Leu Asn Phe Asn Pro Ser Asn Pro Tyr Cys Ala Gly
 355 360 365
 Ile Gln Gly Ile Val Asp Ala Tyr Arg Gln Ala Leu Pro Gln Val Arg
 370 375 380
 Leu Tyr Gly Pro Thr Asn Phe Ala Pro Ile Ile Asn His Val Ala Arg
 385 390 395 400
 Phe Ala Ala Gln Ala Ala His Gln Gly Thr Ala Ser Gln Tyr Phe Met
 405 410 415
 Leu Leu Leu Leu Thr Asp Gly Ala Val Thr Asp Val Glu Ala Thr Arg
 420 425 430
 Glu Ala Val Val Arg Ala Ser Asn Leu Pro Met Ser Val Ile Ile Val
 435 440 445
 Gly Val Gly Gly Ala Asp Phe Glu Ala Met Glu Gln Leu Asp Ala Asp
 450 455 460
 Gly Gly Pro Leu His Thr Arg Ser Gly Gln Ala Ala Ala Arg Asp Ile
 465 470 475 480
 Val Gln Phe Val Pro Tyr Arg Arg Phe Gln Asn Ala Pro Arg Glu Ala
 485 490 495
 Leu Ala Gln Thr Val Leu Ala Glu Val Pro Thr Gln Leu Val Ser Tyr
 500 505 510
 Phe Arg Ala Gln Gly Trp Ala Pro Leu Lys Pro Leu Pro Pro Ser Ala
 515 520 525
 Lys Asp Pro Ala Gln Ala Pro Gln Ala
 530 535

<210> 5

<211> 1114

<212> DNA

<213> Homo sapiens

<220>

<223> integrin B4 binding protein (ITGB4BP)

```

<400> 5
aacggaaacc tttttaggga gtccaaggta cagtcgccgc gtgcggagct tgttactggt 60
tacttggcct catggcggtc cgagcttcgt tgcgagaaca ctgtgagatc ggctgctttg 120
ccaagctcac caacacctac tgtctggtag cgatcggagg ctccagagaac ttctacagtg 180
tgttcgaggg cgagctctcc gataccatcc ccgtgggtgca cgcgtctatc gccggctgcc 240
gcatcatcgg gcgcatgtgt gtgggggaaca ggcacgggtct cctggtagcc aacaatacca 300
ccgaccagga gctgcaacac attcgcaaca gcctcccaga cacagtgcag attaggcggg 360
tggaggagcg gctctcagcc ttgggcaatg tcaccacctg caatgactac gtggccttgg 420
tccacccaga cttggacagg gagacagaag aaattctggc agatgtgctc aagggtggaag 480
tcttcagaca gacagtggcc gaccagggtgc tagtaggaag ctactgtgtc ttcagcaatc 540
agggagggct ggtgcatccc aagacttcaa ttgaagacca ggatgagctg tcctctcttc 600
ttcaagtccc ccttgtggcg gggactgtga accgaggcag tgagggtgatt gctgctggga 660
tggtggtgaa tgactggtgt gccttctgtg gcctggacac aaccagcaca gagctgtcag 720
tgggtggagag tgtcttcaag ctgaatgaag cccagcctag caccattgcc accagcatgc 780
gggattccct cattgacagc ctcacctgag tcaccttcca agttgttcca tgggctcctg 840
gctctggact gtggccaacc ttctccacat tccgccaat ctgtaccgga tgctggcagg 900
gagggtggcag agagctcact gggactgagg ggctgggcac ccaacccttt tccacctgtg 960
cttatcgctt ggatctatca ttactgcaaa aacctgctct gttgtgctgg ctggcaggcc 1020
ctgtggctgc tggctgaggg ttctgctgtc ctgtgccacc ccattaaagt gcagttccct 1080
ccggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1114

```

```

<210> 6
<211> 245
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> integrin B4 binding protein (ITGB4BP)

```

```

<400> 6
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
  1             5             10             15

Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
      20             25             30

Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
      35             40             45

Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
      50             55             60

Gly Asn Arg His Gly Leu Leu Val Pro Asn Asn Thr Thr Asp Gln Glu
      65             70             75             80

Leu Gln His Ile Arg Asn Ser Leu Pro Asp Thr Val Gln Ile Arg Arg
      85             90             95

Val Glu Glu Arg Leu Ser Ala Leu Gly Asn Val Thr Thr Cys Asn Asp
      100            105            110

Tyr Val Ala Leu Val His Pro Asp Leu Asp Arg Glu Thr Glu Glu Ile
      115            120            125

Leu Ala Asp Val Leu Lys Val Glu Val Phe Arg Gln Thr Val Ala Asp
      130            135            140

Gln Val Leu Val Gly Ser Tyr Cys Val Phe Ser Asn Gln Gly Gly Leu
      145            150            155            160

```


<210> 8
 <211> 368
 <212> PRT
 <213> Homo sapiens

<220>
 <223> RNA export protein (RAE1) homolog

<400> 8
 Met Ser Leu Phe Gly Thr Thr Ser Gly Phe Gly Thr Ser Gly Thr Ser
 1 5 10 15
 Met Phe Gly Ser Ala Thr Thr Asp Asn His Asn Pro Met Lys Asp Ile
 20 25 30
 Glu Val Thr Ser Ser Pro Asp Asp Ser Ile Gly Cys Leu Ser Phe Ser
 35 40 45
 Pro Pro Thr Leu Pro Gly Asn Phe Leu Ile Ala Gly Ser Trp Ala Asn
 50 55 60
 Asp Val Arg Cys Trp Glu Val Gln Asp Ser Gly Gln Thr Ile Pro Lys
 65 70 75 80
 Ala Gln Gln Met His Thr Gly Pro Val Leu Asp Val Cys Trp Ser Asp
 85 90 95
 Asp Gly Ser Lys Val Phe Thr Ala Ser Cys Asp Lys Thr Ala Lys Met
 100 105 110
 Trp Asp Leu Ser Ser Asn Gln Ala Ile Gln Ile Ala Gln His Asp Ala
 115 120 125
 Pro Val Lys Thr Ile His Trp Ile Lys Ala Pro Asn Tyr Ser Cys Val
 130 135 140
 Met Thr Gly Ser Trp Asp Lys Thr Leu Lys Phe Trp Asp Thr Arg Ser
 145 150 155 160
 Ser Asn Pro Met Met Val Leu Gln Leu Pro Glu Arg Cys Tyr Cys Ala
 165 170 175
 Asp Val Ile Tyr Pro Met Ala Val Val Ala Thr Ala Glu Arg Gly Leu
 180 185 190
 Ile Val Tyr Gln Leu Glu Asn Gln Pro Ser Glu Phe Arg Arg Ile Glu
 195 200 205
 Ser Pro Leu Lys His Gln His Arg Cys Val Ala Ile Phe Lys Asp Lys
 210 215 220
 Gln Asn Lys Pro Thr Gly Phe Ala Leu Gly Ser Ile Glu Gly Arg Val
 225 230 235 240
 Ala Ile His Tyr Ile Asn Pro Pro Asn Pro Ala Lys Asp Asn Phe Thr
 245 250 255
 Phe Lys Cys His Arg Ser Asn Gly Thr Asn Thr Ser Ala Pro Gln Asp
 260 265 270

Ile Tyr Ala Val Asn Gly Ile Ala Phe His Pro Val His Gly Thr Leu
 275 280 285
 Ala Thr Val Gly Ser Asp Gly Arg Phe Ser Phe Trp Asp Lys Asp Ala
 290 295 300
 Arg Thr Lys Leu Lys Thr Ser Glu Gln Leu Asp Gln Pro Ile Ser Ala
 305 310 315 320
 Cys Cys Phe Asn His Asn Gly Asn Ile Phe Ala Tyr Ala Ser Ser Tyr
 325 330 335
 Asp Trp Ser Lys Gly His Glu Phe Tyr Asn Pro Gln Lys Lys Asn Tyr
 340 345 350
 Ile Phe Leu Arg Asn Ala Ala Glu Glu Leu Lys Pro Arg Asn Lys Lys
 355 360 365

<210> 9

<211> 1878

<212> DNA

<213> Homo sapiens

<220>

<223> bone morphogenetic protein 7 (BMP7)

<400> 9

```

gggcgcagcg gggcccgctct gcagcaagtgc accgacggcc gggacggccg cctgccccct 60
ctgccacctg gggcgggtgcg ggccccggagc ccggagcccc ggtagcgcgt agagccggcg 120
cgatgcacgt gcgctcactg cgagctgcgg cgccgcacag ctctcgtggcg ctctggggcac 180
ccctgttctt gctgcgctcc gccctggccg acttcagcct ggacaacgag gtgcactcga 240
gcttcatcca ccggcgccctc cgcagccagg agcggcgggga gatgcagcgc gagatcctct 300
ccattttggg cttgccccac cgcccgcgcc cgcacctcca gggcaagcac aactcggcac 360
ccatgttcat gctggacctg tacaacgcca tggcgggtgga ggagggcggc gggcccggcg 420
gccaggggctt ctcttaccct tacaaggccg tcttcagtag ccagggcccc cctctggcca 480
gcctgcaaga tagccatttc ctaccgacg ccgacatggt catgagcttc gtcaacctcg 540
tggaacatga caaggaattc ttccaccac gctaccacca tgcagagtgc cggtttgatc 600
tttccaagat ccagaaaggg gaagctgtca cggcagccga attccggatc tacaaggact 660
acatccggga acgcttcgac aatgagacgt tccggatcag cgtttatcag gtgctccagg 720
agcacttggg cagggaatcg gatctcttcc tgctcgacag ccgtaccctc tgggcctcgg 780
aggagggctg gctggtgttt gacatcacag ccaccagcaa ccaactgggt gtcaatccgc 840
ggcacaacct gggcctgcag ctctcgggtg agacgttggg tgggcagagc atcaacccca 900
agttggcggg cctgattggg cggcacgggc ccagaacaa gcagcccttc atggtggctt 960
tcttcaaggc cagggaggtc cacttccgca gcatccggtc cagggggagc aaacagcgca 1020
gccagaaccg ctccaagacg cccaagaacc aggaagccct gcggatggcc aacgtggcag 1080
agaacagcag cagcgaccag aggcaggcct gtaagaagca cgagctgtat gtcagcttcc 1140
gagacctggg ctggcaggac tggatcatcg cgctgaagg ctacgccgcc tactactgtg 1200
agggggagtg tgccttcctt ctgaactcct acatgaacgc caccaaccac gccatcgtgc 1260
agacgttgtt ccacttcata aaccgggaaa cgggtgcccc ggcctgctgt gcgcccacgc 1320
agctcaatgc catctccgtc ctctacttcg atgacagctc caacgtcatc ctgaagaaat 1380
acagaaacat ggtggtccgg gcctgtggct gccactagct cctccgagaa ttcagaccct 1440
ttggggccaa gtttttctgg atcctccatt gctcgccttg gccaggaacc agcagaccaa 1500
ctgccttttg tgagaccttc ccctccctat ccccaacttt aaagggtgtg gagtattagg 1560
aaacatgagc agcatatggc ttttgatcag tttttcagtg gcagcatcca atgaacaaga 1620
tcttacaagc tgtgcaggca aaacctagca ggaaaaaaa acaacgcata aagaaaaatg 1680
gccggggccag gtcattggct gggaagtctc agccatgcac ggactcgttt ccagaggtaa 1740
ttatgagcgc ctaccagcca ggccaccag ccgtgggagg aagggggcgt ggcaagggtt 1800
gggcacattg gtgtctgtgc gaaaggaaaa ttgaccggga agttcctgta ataatgtca 1860
caataaaacg aatgaatg

```

<210> 10
 <211> 431
 <212> PRT
 <213> Homo sapiens

<220>
 <223> bone morphogenetic protein 7 (BMP7)

<400> 10
 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30
 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45
 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60
 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80
 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
 85 90 95
 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
 100 105 110
 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
 115 120 125
 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
 130 135 140
 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
 145 150 155 160
 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270

Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

<210> 11

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<223> guanine nucleotide binding protein (G protein),
 alpha stimulating activity polypeptide 1 (GNAS)

<400> 11

ccgcccgcgc cgcagcccgc cgcgcgccgc ccgcccgcgc cgcgcgccatg ggctgcctcg 60
 ggaacagtaa gaccgaggac cagcgcaacg aggagaaggc gcagcgtgag gccacaacaaa 120
 agatcgagaa gcagctgcag aaggacaagc aggtctaccg ggccacgcac cgcctgctgc 180
 tgctgggtgc tggagaatct ggtaaaagca ccattgtgaa gcagatgagg atcctgcatg 240
 ttaatgggtt taatggagag ggcggcgaag aggacccgca ggctgcaagg agcaacagcg 300
 atggtgagaa ggcaacacaa gtgcaggaca tcaaaaacaa cctgaaagag gcgattgaaa 360
 ccattgtggc cgccatgagc aacctggtgc cccccgtgga gctggccaac cccgagaacc 420
 agttcagagt ggactacatc ctgagtgtga tgaacgtgcc tgactttgac ttccctccc 480
 aattctatga gcatgccaag gctctgtggg aggatgaagg agtgcgtgcc tgctacgaac 540
 gctccaacga gtaccagctg attgactgtg cccagtactt cctggacaag atcgacgtga 600
 tcaagcaggc tgactatgtg ccgagcgatc aggacctgct tcgctgccgt gtccctgactt 660
 ctggaatctt tgagaccaag ttccaggtgg acaaagtcaa ctccacatg tttgacgtgg 720
 gtggccagcg cgatgaacgc cgcaagtgga tccagtgtt caacgatgtg actgccatca 780
 tcttcgtggt ggccagcagc agctacaaca tggctcatccg ggaggacaac cagaccaacc 840
 gcttcgagga ggctctgaac ctcttcaaga gcatctggaa caacagatgg ctgcgcacca 900
 tctctgtgat cctgttcctc aacaagcaag atctgctcgc tgagaaagtc cttgctggga 960
 aatcgaagat tgaggactac tttccagaat ttgctcgcta cactactcct gaggatgcta 1020
 ctcccgagcc cggagaggac ccacgcgtga cccgggccaa gtacttcatt cgagatgagt 1080
 ttctgaggat cagcactgcc agtggagatg ggcgtcacta ctgctaccct catttcacct 1140
 gcgctgtgga cactgagaac atccgccgtg tgttcaacga ctgccgtgac atcattcagc 1200

```

gcatgcacct tcgtcagtac gagctgctct aagaagggaa cccccaatt taattaaagc 1260
cttaagcaca attaattaa agtgaaacgt aattgtacaa gcagttaatc acccaccata 1320
gggcatgatt aacaaagcaa cctttccctt ccccgagtg attttgcgaa accccctttt 1380
cccttcagct tgcttagatg ttccaaattt agaaagctta aggcggccta cagaaaaagg 1440
aaaaaaggcc acaaaagttc cctctcactt tcagtaaaaa taaataaaac agcagcagca 1500
aacaataaaa atgaaataaa agaaacaaat gaaataaata ttgtgttggtg cagcattaa 1560
aaaaatcaaa ataaaaatta aatgtgagca aag 1593

```

```

<210> 12
<211> 394
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> guanine nucleotide binding protein (G protein),
      alpha stimulating activity polypeptide 1 (GNAS)

```

```

<400> 12
Met Gly Cys Leu Gly Asn Ser Lys Thr Glu Asp Gln Arg Asn Glu Glu
  1             5             10             15

Lys Ala Gln Arg Glu Ala Asn Lys Lys Ile Glu Lys Gln Leu Gln Lys
      20             25             30

Asp Lys Gln Val Tyr Arg Ala Thr His Arg Leu Leu Leu Leu Gly Ala
      35             40             45

Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His
      50             55             60

Val Asn Gly Phe Asn Gly Glu Gly Gly Glu Glu Asp Pro Gln Ala Ala
      65             70             75             80

Arg Ser Asn Ser Asp Gly Glu Lys Ala Thr Lys Val Gln Asp Ile Lys
      85             90             95

Asn Asn Leu Lys Glu Ala Ile Glu Thr Ile Val Ala Ala Met Ser Asn
      100            105            110

Leu Val Pro Pro Val Glu Leu Ala Asn Pro Glu Asn Gln Phe Arg Val
      115            120            125

Asp Tyr Ile Leu Ser Val Met Asn Val Pro Asp Phe Asp Phe Pro Pro
      130            135            140

Glu Phe Tyr Glu His Ala Lys Ala Leu Trp Glu Asp Glu Gly Val Arg
      145            150            155            160

Ala Cys Tyr Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln
      165            170            175

Tyr Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val Pro
      180            185            190

Ser Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe
      195            200            205

Glu Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val
      210            215            220

```

Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp
 225 230 235 240
 Val Thr Ala Ile Ile Phe Val Val Ala Ser Ser Ser Tyr Asn Met Val
 245 250 255
 Ile Arg Glu Asp Asn Gln Thr Asn Arg Leu Gln Glu Ala Leu Asn Leu
 260 265 270
 Phe Lys Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Val Ile
 275 280 285
 Leu Phe Leu Asn Lys Gln Asp Leu Leu Ala Glu Lys Val Leu Ala Gly
 290 295 300
 Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Phe Ala Arg Tyr Thr Thr
 305 310 315 320
 Pro Glu Asp Ala Thr Pro Glu Pro Gly Glu Asp Pro Arg Val Thr Arg
 325 330 335
 Ala Lys Tyr Phe Ile Arg Asp Glu Phe Leu Arg Ile Ser Thr Ala Ser
 340 345 350
 Gly Asp Gly Arg His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp
 355 360 365
 Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln
 370 375 380
 Arg Met His Leu Arg Gln Tyr Glu Leu Leu
 385 390

<210> 13
 <211> 1439
 <212> DNA
 <213> Homo sapiens

<220>
 <223> eukaryotic translation initiation factor 2,
 subunit 2 beta (EIF2S2)

<400> 13
 ggggtgtcgt ttcctttcgc tgatgcaaga gcctagtgcg gtggtgggag aggtatcggc 60
 aggggcagcg ctgccgccgg ggccctggggc tgaccctgtct gacttcccgt ccgtgccgag 120
 cccactcgag ccgcagccat gtctggggac gagatgattt ttgatccctac tatgagcaag 180
 aagaaaaaga agaagaagaa gcctttttatg ttagatgagg aaggggatac ccaaacagag 240
 gaaacccagc cttcagaaac aaaagaagtg gagccagagc caactgagga caaggatttg 300
 gaagctgatg aagaggacac taggaaaaaa gatgcttctg atgatctaga tgacttgaac 360
 ttctttaatc aaaagaaaaa gaagaaaaaa actaaaaaga tatttgatat tgatgaagct 420
 gaagaagggt taaaggatct taagattgaa agtgatgttc aagaaccaac tgaaccagag 480
 gatgaccttg acattatgct tggcaataaa aagaagaaaa agaagaatgt taagtccca 540
 gatgaggatg aaataactaga gaaagatgaa gctctagaag atgaagacaa caaaaaagat 600
 gatggtatct cattcagtaa tcagacaggc cctgcttggg caggctcaga aagagactac 660
 acatacgagg agctgctgaa tcgagtgttc aacatcatga gggaaaagaa tccagatatg 720
 gttgctgggg agaaaaggaa atttgtcatg aaacctccac aagtcgtccg agtaggaacc 780
 aagaaaaactt cttttgtcaa ctttacagat atctgtaaac tattacatcg tcagcccaaa 840
 catctccttg catttttgtt ggctgaattg ggtacaagtg gttctataga tggtaataac 900
 caacttgtaa tcaaaggaag attccaacag aaacagatag aaaatgtctt gagaagatat 960
 atcaaggaat atgtcacttg tcacacatgc cgatcaccgg acacaatcct gcagaaggac 1020

```

acacgactct atttcctaca gtgcgaaact tgtcattcta gatgttctgt tgccagtatc 1080
aaaaccggct tccaggctgt cacgggcaag cgagcacagc tccgtgccaa agctaactaa 1140
tttgctaatac actgattttg caaagcttgt tgtggagatg tggctggaca ggtttgccat 1200
cagagtggat ataccgttgt attaaaaaca agataaaaaa gctgccaaga tttttggcga 1260
gtggttggtc tgaagtcctt gcaagacgct gatgctcaag ctgttgacat actcattgcc 1320
tactttaaca cctgtcagag aaacgtgata tggggtaagg aggtgctttt ttaaaatcgt 1380
tcatagactt ctgtaaaatg caagataaat taaagttatt ataacagtga ttctttcaa 1439

```

<210> 14

<211> 333

<212> PRT

<213> Homo sapiens

<220>

<223> eukaryotic translation initiation factor 2,
subunit 2 beta (EIF2S2)

<400> 14

```

Met Ser Gly Asp Glu Met Ile Phe Asp Pro Thr Met Ser Lys Lys Lys
  1              5              10              15

Lys Lys Lys Lys Lys Pro Phe Met Leu Asp Glu Glu Gly Asp Thr Gln
          20              25              30

Thr Glu Glu Thr Gln Pro Ser Glu Thr Lys Glu Val Glu Pro Glu Pro
  35              40              45

Thr Glu Asp Lys Asp Leu Glu Ala Asp Glu Glu Asp Thr Arg Lys Lys
  50              55              60

Asp Ala Ser Asp Asp Leu Asp Asp Leu Asn Phe Phe Asn Gln Lys Lys
  65              70              75              80

Lys Lys Lys Lys Thr Lys Lys Ile Phe Asp Ile Asp Glu Ala Glu Glu
          85              90              95

Gly Val Lys Asp Leu Lys Ile Glu Ser Asp Val Gln Glu Pro Thr Glu
          100              105              110

Pro Glu Asp Asp Leu Asp Ile Met Leu Gly Asn Lys Lys Lys Lys Lys
          115              120              125

Lys Asn Val Lys Phe Pro Asp Glu Asp Glu Ile Leu Glu Lys Asp Glu
          130              135              140

Ala Leu Glu Asp Glu Asp Asn Lys Lys Asp Asp Gly Ile Ser Phe Ser
          145              150              155              160

Asn Gln Thr Gly Pro Ala Trp Ala Gly Ser Glu Arg Asp Tyr Thr Tyr
          165              170              175

Glu Glu Leu Leu Asn Arg Val Phe Asn Ile Met Arg Glu Lys Asn Pro
          180              185              190

Asp Met Val Ala Gly Glu Lys Arg Lys Phe Val Met Lys Pro Pro Gln
          195              200              205

Val Val Arg Val Gly Thr Lys Lys Thr Ser Phe Val Asn Phe Thr Asp
          210              215              220

```

Ile Cys Lys Leu Leu His Arg Gln Pro Lys His Leu Leu Ala Phe Leu
 225 230 235 240
 Leu Ala Glu Leu Gly Thr Ser Gly Ser Ile Asp Gly Asn Asn Gln Leu
 245 250 255
 Val Ile Lys Gly Arg Phe Gln Gln Lys Gln Ile Glu Asn Val Leu Arg
 260 265 270
 Arg Tyr Ile Lys Glu Tyr Val Thr Cys His Thr Cys Arg Ser Pro Asp
 275 280 285
 Thr Ile Leu Gln Lys Asp Thr Arg Leu Tyr Phe Leu Gln Cys Glu Thr
 290 295 300
 Cys His Ser Arg Cys Ser Val Ala Ser Ile Lys Thr Gly Phe Gln Ala
 305 310 315 320
 Val Thr Gly Lys Arg Ala Gln Leu Arg Ala Lys Ala Asn
 325 330

<210> 15
 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <223> dynein light chain A2 (DNCL2A)

<400> 15
 cgcagaaagg cacaggactc gctaagtgtt cgctacgcgg ggctaccgga tcggtcggaa 60
 atggcagagg tggaggagac actgaagcga ctgcagagcc agaagggagt gcagggaatc 120
 atcgctcgtga acacagaagg cattcccatc aagagcacca tggacaaccc caccaccacc 180
 cagtatgccg gcctcatgca cagcttcatc ctgaaggcac ggagcaccgt gcgtgacatc 240
 gacccccaga acgatctcac cttccttcga attcgctcca agaaaaatga aattatgggt 300
 gcaccagata aagactatct cctgattgtg attcagaatc caaccgaata agccactctc 360
 ttggctccct gtgtcattcc ttaatttaat gccccccaag aatgttaatg tcaatcatgt 420
 cagtggacta gcacatggca gtcgcttgga acccactcac accaatccag tgaccgtgtg 480
 tgggctggcg gctcttctcc cccaccaacg gaacctctgt gtgcaccaac cttccccaga 540
 gctccggagc gccctctcct cacttccagg ttttggagca agagcttgca ggaagccgcg 600
 acccagcttc cttctgacct tcagttcaact ttgtcgccct tggagaaagc tgtttttctt 660
 taactaaaaa taaccaaaat gcttaaaaaa aaaaaaaaaa aa 702

<210> 16
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <223> dynein light chain A2 (DNCL2A)

<400> 16
 Met Ala Glu Val Glu Glu Thr Leu Lys Arg Leu Gln Ser Gln Lys Gly
 1 5 10 15
 Val Gln Gly Ile Ile Val Val Asn Thr Glu Gly Ile Pro Ile Lys Ser
 20 25 30

Thr Met Asp Asn Pro Thr Thr Thr Gln Tyr Ala Ser Leu Met His Ser
35 40 45

Phe Ile Leu Lys Ala Arg Ser Thr Val Arg Asp Ile Asp Pro Gln Asn
50 55 60

Asp Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys Asn Glu Ile Met Val
65 70 75 80

Ala Pro Asp Lys Asp Tyr Phe Leu Ile Val Ile Gln Asn Pro Thr Glu
85 90 95

<210> 17
<211> 984
<212> DNA
<213> Homo sapiens

<220>
<223> proteasome subunit alpha-7 (PSMA7)

<400> 17
cggcgccgag ggtggggcgc gggcgtagtg gcgcggggag tcgcgggtgc gcgcggggccg 60
tgagtgtgcg cttttgagag tcgcggcgga aggagcccgg ccgcgcggccg ccggcatgag 120
ctacgaccgc gccatcaccg tcttctcgcc cgacggccac ctcttccaag tggagtacgc 180
gcaggaggcc gtcaagaagg gctcgaccgc ggttggtggt cgaggaagag acattgttgt 240
tcttggtgtg gagaagaagt cagtggccaa actgcaggat gaaagaacag tgcggaagat 300
ctgtgctttg gatgacaacg tctgcatggc ctttgcaggc ctcaccgccg atgcaaggat 360
agtcatcaac agggcccggg tggagtgccg gagccaccgg ctgactgtgg aggaccgggt 420
cactgtggag tacatcaccg gctacatcgc cagtctgaag cagcggtata cgcagagcaa 480
tgggcgcagg ccgtttggca tctctgccct catcgtgggt ttcgactttg atggcactcc 540
taggctctat cagactgacc cctcgggac ataccatgcc tgggaaggcca atgccatagg 600
tcggggtgcc aagtcagtgc gcgagttcct ggagaagaac tatactgacg aagccattga 660
aacagatgat ctgaccatta agctggtgat caaggcactc ctggaagtgg ttcagtcagg 720
tggcaaaaac attgaacttg ctgtcatgag gcgagatcaa tccctcaaga ttttaaattcc 780
tgaagaaatt gagaagtatg ttgctgaaat tgaaaaagaa aaagaagaaa acgaaaagaa 840
gaaacaaaag aaagcatcat gatgaataaa atgtctttgc ttgtaatttt taaattcata 900
tcaatcatgg atgagtctcg atgtgtaggc ctttccattc catttattca cactgagtgt 960
cctacaataa acttccgtat tttt 984

<210> 18
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<223> proteasome subunit alpha-7 (PSMA7)

<400> 18
Met Ser Tyr Asp Arg Ala Ile Thr Val Phe Ser Pro Asp Gly His Leu
1 5 10 15

Phe Gln Val Glu Tyr Ala Gln Glu Ala Val Lys Lys Gly Ser Thr Ala
20 25 30

Val Gly Val Arg Gly Arg Asp Ile Val Val Leu Gly Val Glu Lys Lys
35 40 45

Ser Val Ala Lys Leu Gln Asp Glu Arg Thr Val Arg Lys Ile Cys Ala
50 55 60

Leu Asp Asp Asn Val Cys Met Ala Phe Ala Gly Leu Thr Ala Asp Ala
 65 70 75 80
 Arg Ile Val Ile Asn Arg Ala Arg Val Glu Cys Gln Ser His Arg Leu
 85 90 95
 Thr Val Glu Asp Pro Val Thr Val Glu Tyr Ile Thr Arg Tyr Ile Ala
 100 105 110
 Ser Leu Lys Gln Arg Tyr Thr Gln Ser Asn Gly Arg Arg Pro Phe Gly
 115 120 125
 Ile Ser Ala Leu Ile Val Gly Phe Asp Phe Asp Gly Thr Pro Arg Leu
 130 135 140
 Tyr Gln Thr Asp Pro Ser Gly Thr Tyr His Ala Trp Lys Ala Asn Ala
 145 150 155 160
 Ile Gly Arg Gly Ala Lys Ser Val Arg Glu Phe Leu Glu Lys Asn Tyr
 165 170 175
 Thr Asp Glu Ala Ile Glu Thr Asp Asp Leu Thr Ile Lys Leu Val Ile
 180 185 190
 Lys Ala Leu Leu Glu Val Val Gln Ser Gly Gly Lys Asn Ile Glu Leu
 195 200 205
 Ala Val Met Arg Arg Asp Gln Ser Leu Lys Ile Leu Asn Pro Glu Glu
 210 215 220
 Ile Glu Lys Tyr Val Ala Glu Ile Glu Lys Glu Lys Glu Glu Asn Glu
 225 230 235 240
 Lys Lys Lys Gln Lys Lys Ala Ser
 245

<210> 19

<211> 4713

<212> DNA

<213> Homo sapiens

<220>

<223> activity dependent neuroprotective protein (ADNP)

<400> 19

cggccgcggc gcgagccgga gtccgcccag cgggagcgcg acgaggcccc gggcgcgccc 60
 tccccgctgc cgccaccgcc gtgccgcgcg catccgcccg ccgccgcgcg cgctgtccgg 120
 cccccgagca cgccggcccc gcgcgcgcct cgaggccgag tcaagggtgtg agatgcacaa 180
 tgcgaaacct aggccccagc ttttacacca tgatgcgcag gggtgtactt tttgtactga 240
 actgataggt ggcctagtgg ttatgccttg tactaccatt ttgaggatct ggactccgtt 300
 tcttgccctg ctctttggac cacattgtca attcacaccg aaactatgtt ccaacttcct 360
 gtcaacaatc ttggcagttt aagaaaagcc cggaaaactg tgaaaaaat acttagtgac 420
 attgggttgg aatactgtaa agaacaatata gaagatttta aacaatttga acctaattgac 480
 ttttatttga aaaacactac atgggaggat gtaggactgt gggacccatc acttacgaaa 540
 aaccaggact atcggacaaa acctttctgc tgcagcgctt gtccattttc ctcaaaattc 600
 ttctctgcct acaaaagtca tttccgcaat gtccatagtg aagactttga aaataggatt 660
 ctcccttaatt gccctactg taccttcaat gcagacaaaa agacttttga aacacacatt 720
 aaaatatattc atgctccgaa cgccagcgca ccaagtagca gcctcagcac tttcaaagat 780
 aaaaacaaaa atgatggcct taaacctaag caggctgaca gtgtagagca agctgtttat 840
 tactgtaaga agtgactta ccgagatcct ctttatgaaa tagttaggaa gcacatttac 900

agggaaacatt	ttcagcatgt	ggcagcacct	tacatagcaa	aggcaggaga	aaaatcactc	960
aatggggcag	tccccttagg	ctcgaatgcc	cgagaagaga	gtagtattca	ctgcaagcga	1020
tgccttttca	tgccaaagtc	ctatgaagct	ttggtagacg	atgtcatcga	agaccatgaa	1080
cgatataggct	atcagggtcac	tgccatgatt	gggcacacaa	atgtagtggg	tccccgatcc	1140
aaacccttga	tgctaattgc	tcccaaacct	caagacaaga	agagcatggg	actcccacca	1200
aggatcggtt	cccttgcttc	tggaaatgtc	cggctctttac	catcacagca	gatgggtgaat	1260
cgactctcaa	taccaaagcc	taacttaaat	tctacaggag	tcaacatgat	gtccagtggt	1320
catctgcagc	agaacaacta	tggagtcaaa	tctgtaggcc	agggttacag	tgttggtcag	1380
tcaatgagac	tgggtctagg	tggcaacgca	ccagtttcca	ttcctcaaca	atctcagttc	1440
gtaaagcagt	tacttccaag	tggaaacgga	aggtcttatg	ggcttgggtc	agagcagagg	1500
tcccaggcac	cagcaagata	ctccctgcag	tctgctaattg	cctcttctct	ctcatcgggc	1560
cagttaaagt	ctccttccct	ctctcagtca	caggcatcca	gagtgttagg	tcagttcagt	1620
tccaaacctg	ctgcagctgc	cacaggccct	cccccaggta	acacttcctc	aactcaaaaag	1680
tggaaaatat	gtacaatctg	taatgagctt	tttctgaaa	atgtctatag	tgtgcacttc	1740
gaaaaagaac	ataaagctga	gaaagtccca	gcagtagcca	actacattat	gaaaatacac	1800
aattttacta	gcaaatgcct	ctactgtaat	cgctattttac	ccacagatac	tctgctcaac	1860
catatgttaa	ttcatgggtc	gtcttgtcca	tattgcccgtt	caactttcaa	tgatgtggaa	1920
aagatggccg	cacacatgcg	gatggttcac	attgatgaag	agatggggacc	taaaacagat	1980
tctactttga	gttttgattt	gacattgcag	cagggtagtc	acactaacat	ccatctcctg	2040
gtaactacat	acaatctgag	ggatgcccc	gctgaatctg	ttgcttacca	tgcccaaaaat	2100
aatcctccag	ttcctccaaa	gccacagcca	aagggtcagg	aaaaggcaga	tatccctgta	2160
aaaagttcac	ctcaagctgc	agtgccttat	aaaaaagatg	ttgggaaaac	cctttgtcct	2220
ctttgctttt	caatcctaaa	aggacccata	tctgatgcac	ttgcacatca	cttacgagag	2280
aggcaccaag	ttattcagac	ggttcatcca	gttgagaaaa	agctcaccta	caaagtgtatc	2340
cattgccttg	gtgtgtatac	cagcaacatg	accgcctcaa	ctatcactct	gcacttagtt	2400
cactgcaggg	gcgttggaag	gacccaaaat	ggccaggata	agacaaatgc	accctctcgg	2460
cttaatcagt	ctccaagtct	ggcacctgtg	aagcgcactt	acgagcaaat	ggaatttccc	2520
ttactgaaaa	aacgaaagtt	agatgatgat	agtgattcac	ccagcttctt	tgaagagaag	2580
cctgaagagc	ctgttgtttt	agctttagac	cccaagggtc	atgaagatga	ttcctatgaa	2640
gccaggaaaa	gctttctaaa	aaagtatttc	aacaaacagc	cctatcccac	caggagagaa	2700
attgagaagc	tagcagccag	tttatgggtt	tggaaagatg	acatcgcttc	ccattttagt	2760
aacaaaagga	agaagtgtgt	ccgtgattgt	gaaaagtaca	agcctggcgt	gttgctgggg	2820
tttaacatga	aagaattaaa	taaagtcaag	catgagatgg	attttgatgc	tgagtggcta	2880
tttgaaaatc	atgatgagaa	ggattccaga	gtcaatgcta	gtaagactgc	tgacaaaaag	2940
ctcaaccttg	ggaagggaag	tgacagttcc	tcagacagtt	ttgaaaattt	ggaagaagaa	3000
tccaatgaaa	gtggtagccc	ttttgaccct	gtttttgaag	ttgaacctaa	aatctctaac	3060
gataaccacg	aggaacatgt	actgaaggta	attcctgagg	atgcttcaga	atctgaggag	3120
aagctagacc	aaaaagagga	tggttcaaaa	tacgaaacta	ttcatttgac	tgaggaacca	3180
accaaactaa	tgcacaatgc	atctgatagt	cagggttgacc	aagacgatgt	tgttgatggg	3240
aaagacgggtg	ctctccatc	tgcagatggg	ctgggatccc	aacaagtgtc	agactttgag	3300
gacaatacct	gcgaaatgaa	accaggaacc	tggctctgacg	agtcttccca	aagcgaagat	3360
gcaaggagca	gtaagccagc	tgccaaaaaa	aaggctacca	tgcaagggtga	cagagagcag	3420
ttgaaatgga	agaatagttc	ctatggaaaa	gttgaagggt	tttgggtctaa	ggaccagtca	3480
cagtggaaga	atgcatctga	gaatgatgag	cgcttatcta	acccccagat	tgagtggcag	3540
aatagcacia	ttgacagtga	ggatggggaa	cagtttgaca	acatgactga	tggagttagct	3600
gagcccatgc	atggcagctt	agccggagtt	aaactgagca	gccaacaggc	ctaagtgcc	3660
ggttccctgg	cgttgggtgac	atgctgcagc	ctggaactct	gatctccagt	gtgactgcaa	3720
agctgtcttc	tcactggtac	tgccttggtga	gtactgggtg	gactgtgggg	catgtggccg	3780
ctgcagttcc	agtggttatt	tctaagtcta	tgacaggaca	ggctgttctt	gcttcagaac	3840
cttctctgac	agacacggta	actaaatgtg	aaaaaccaat	aagctgggtga	ctcatgaata	3900
cacacgagga	aaagcagagg	tttattttat	ctgccttttc	aacatttctt	tccctctgtg	3960
aaatgattgg	tcagatgtct	ttgagaagtg	ttaaactaat	tcacatggta	gtgtagggcc	4020
aacatacaag	ctaccagtct	aatgtgtata	gtagactttg	ggaaaagcga	ttttttttca	4080
tgtattcatt	ctgaatagtt	gaaatgtata	tttgtagagt	cttttagacc	tattcaagtg	4140
atgctcatga	tctgtttact	gtgtgccc	catagatttc	tttttttagt	gttgcccttg	4200
ctgtgtaata	aacgctctat	ctagttttacc	tagcaaaaagc	tcaaaaactgc	gctagtagtg	4260
actttttgga	cagacttagt	ttttgcacat	aaccttgtag	aatcttgcaa	cagagggccg	4320
ccacgtaaag	tatatatctg	gactctcttg	tattatagga	tttttcttgt	tctgaatatc	4380
cttgacatta	cagctgtcaa	aaacaaaaaac	tggatatttca	gatctgtttt	ctgaaatctt	4440
ttaaagctaaa	atcacatgca	agaattgact	ttgcagctac	taatttttgac	acctttttaga	4500
tctgtataaa	agtgtgttgt	gttgaagcag	caaaccaatg	agtgtgtcat	tttggatatt	4560

tagttttatc ttttagttcaa caccatcatg gtggattcat ttataccatc taatatatga 4620
cacactgttg tagtatgtat aattttgtga tctttatttt ccctttgtat tcattttaag 4680
catctaaata aattgctgta ttgtgcttaa tgt 4713

<210> 20
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
<223> activity dependent neuroprotective protein (ADNP)

<400> 20
Met Phe Gln Leu Pro Val Asn Asn Leu Gly Ser Leu Arg Lys Ala Arg
1 5 10 15
Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
20 25 30
Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
35 40 45
Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
50 55 60
Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65 70 75 80
Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
85 90 95
His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
100 105 110
Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
115 120 125
His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
130 135 140
Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145 150 155 160
Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
165 170 175
Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
180 185 190
Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
195 200 205
Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
210 215 220
Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225 230 235 240
Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
245 250 255

His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
 260 265 270
 Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
 275 280 285
 Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
 290 295 300
 Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
 305 310 315 320
 Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
 325 330 335
 Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
 340 345 350
 Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
 355 360 365
 Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
 370 375 380
 Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
 385 390 395 400
 Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
 405 410 415
 Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
 420 425 430
 Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
 435 440 445
 Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
 450 455 460
 Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
 465 470 475 480
 Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
 485 490 495
 Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
 500 505 510
 Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
 515 520 525
 Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
 530 535 540
 Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
 545 550 555 560
 Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
 565 570 575

Glu	Ser	Val	Ala	Tyr	His	Ala	Gln	Asn	Asn	Pro	Pro	Val	Pro	Pro	Lys	
			580					585					590			
Pro	Gln	Pro	Lys	Val	Gln	Glu	Lys	Ala	Asp	Ile	Pro	Val	Lys	Ser	Ser	
		595					600					605				
Pro	Gln	Ala	Ala	Val	Pro	Tyr	Lys	Lys	Asp	Val	Gly	Lys	Thr	Leu	Cys	
	610					615					620					
Pro	Leu	Cys	Phe	Ser	Ile	Leu	Lys	Gly	Pro	Ile	Ser	Asp	Ala	Leu	Ala	
625					630					635					640	
His	His	Leu	Arg	Glu	Arg	His	Gln	Val	Ile	Gln	Thr	Val	His	Pro	Val	
				645					650					655		
Glu	Lys	Lys	Leu	Thr	Tyr	Lys	Cys	Ile	His	Cys	Leu	Gly	Val	Tyr	Thr	
			660					665					670			
Ser	Asn	Met	Thr	Ala	Ser	Thr	Ile	Thr	Leu	His	Leu	Val	His	Cys	Arg	
		675					680					685				
Gly	Val	Gly	Lys	Thr	Gln	Asn	Gly	Gln	Asp	Lys	Thr	Asn	Ala	Pro	Ser	
	690					695					700					
Arg	Leu	Asn	Gln	Ser	Pro	Ser	Leu	Ala	Pro	Val	Lys	Arg	Thr	Tyr	Glu	
705					710					715					720	
Gln	Met	Glu	Phe	Pro	Leu	Leu	Lys	Lys	Arg	Lys	Leu	Asp	Asp	Asp	Ser	
				725					730					735		
Asp	Ser	Pro	Ser	Phe	Phe	Glu	Glu	Lys	Pro	Glu	Glu	Pro	Val	Val	Leu	
			740					745					750			
Ala	Leu	Asp	Pro	Lys	Gly	His	Glu	Asp	Asp	Ser	Tyr	Glu	Ala	Arg	Lys	
		755					760					765				
Ser	Phe	Leu	Thr	Lys	Tyr	Phe	Asn	Lys	Gln	Pro	Tyr	Pro	Thr	Arg	Arg	
	770					775					780					
Glu	Ile	Glu	Lys	Leu	Ala	Ala	Ser	Leu	Trp	Leu	Trp	Lys	Ser	Asp	Ile	
785					790					795					800	
Ala	Ser	His	Phe	Ser	Asn	Lys	Arg	Lys	Lys	Cys	Val	Arg	Asp	Cys	Glu	
				805					810					815		
Lys	Tyr	Lys	Pro	Gly	Val	Leu	Leu	Gly	Phe	Asn	Met	Lys	Glu	Leu	Asn	
			820					825					830			
Lys	Val	Lys	His	Glu	Met	Asp	Phe	Asp	Ala	Glu	Trp	Leu	Phe	Glu	Asn	
		835					840					845				
His	Asp	Glu	Lys	Asp	Ser	Arg	Val	Asn	Ala	Ser	Lys	Thr	Ala	Asp	Lys	
	850					855					860					
Lys	Leu	Asn	Leu	Gly	Lys	Glu	Asp	Asp	Ser	Ser	Ser	Asp	Ser	Phe	Glu	
865					870					875					880	
Asn	Leu	Glu	Glu	Glu	Ser	Asn	Glu	Ser	Gly	Ser	Pro	Phe	Asp	Pro	Val	
				885					890					895		

Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
900 905 910
Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
915 920 925
Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
930 935 940
Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945 950 955 960
Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
965 970 975
Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
980 985 990
Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser
995 1000 1005
Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu
1010 1015 1020
Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp
1025 1030 1035 1040
Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg
1045 1050 1055
Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu
1060 1065 1070
Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met
1075 1080 1085
His Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
1090 1095 1100

<210> 21

<211> 2427

<212> DNA

<213> Homo sapiens

<220>

<223> chromosome 20 open reading frame 129 (C20orf129)
protein

<400> 21

aaaaagcagc caatgggaga gccgaggcgg ggaggtgcgg ccaatggcgc gggcctgttt 60
gattcaaagg ttgcctataa agcgggactg cacgccggtt tttgtccgag ggctgtcgag 120
tccgagcgcc gccatggctc tgctgtccga gggcctggac gaggtgcccg ccgcctgcct 180
gtcgccgtgc gggccgcca acccgaccga gctgttcagc gagtcacggc gcctggctct 240
ggaggagctg gtggcgggcg gcccgaagc cttcgcgccg ttctgcgac gcgagcgct 300
ggctcgtttc ctgaaccccg atgaggtgca cgccattctg cgcgcgcgcg agaggccggg 360
agaggagggc gcgcgggcgg cgcgggcgcc cgaggactcg ttcggctcct cgcacgactg 420
ctcttcgggc acctacttcc ccgagcagtc ggacctggag ccaccgctgt tggagcttgg 480
ctggcccgcc ttctaccagg gcgcctaccg cggcgccacg cgtgtcgaga cgcacttcca 540
gccccgcggc gctggcgaag gtggccccta cggctgcaag gacgctctgc gccagcagct 600
ccgctcggcg cgagaggtga ttgcagtggc catggacgtg ttcacagaca tcgacatctt 660

```

cagagacctg caagaaatat gcaggaaaca gggagttgct gtgtatatcc ttctggacca 720
ggctctcctc tctcaatttc tggatatgtg catggatctg aaagttcatc ctgaacagga 780
aaagttaatg acagttcggg ctatcacagg aaatatctac tatgcaaggt caggaactaa 840
gattattggg aaggttcacg aaaagttcac gttgattgat ggcatccgcg tggcaacagg 900
ctcctacagt tttaacataga cggatggcaa attaaacagc agtaacttgg taattctgtc 960
tggccaagtg gttgaacact ttgatctgga gttccgaatc ctgtatgccc agtccaagcc 1020
catcagcccc aaactcctgt ctacttcca gagcagcaac aagtttgatc acctcaccaa 1080
ccgaaaacca cagtccaagg agctcaccct gggcaacctg ctgcggatgc ggctggctag 1140
gctgtcaagt actcccagga aggcggacct ggacccagag atgcccgcag agggcaaggc 1200
agagcgcaag ccccatgact gtgagtcctc tactgttagt gaggaagact acttcagcag 1260
ccacagggac gagctccaga gcagaaaggc cattgacgct gccactcaaa cagagccagg 1320
agaggagatg ccagggtgta gtgtgagtga ggtgggaaca caaaccagca tcaccacagc 1380
atgtgctggg acccagactg cagtcatcac caggatagca agctctcaaa ccacgatttg 1440
gtccagatcg accactactc agactgacat ggtatgagaac attctctttc ctcgaggaac 1500
tcaatctaca gaagggtcac cagtctcaaa aatgtctgta tcgagatctt ccagtttgaa 1560
gtcttcctcc tctgtgtctt cccaaggctc tgtggcaagc tccactgggt ctcccgttc 1620
catcagaacc actgacttcc acaatcctgg ctatcccaag tacctgggca cccccacct 1680
ggaactgtac ttgagtgact cacttagaaa cttgaacaaa gagcggcaat tccacttcgc 1740
tggtatcagg tcccggctca accacatgct ggctatgctg tcaaggagaa cactctttac 1800
tgaaaaccac cttggccttc attctggcaa tttcagcaga gttaatttgc ttgctgtag 1860
agatgtagca ctttatcctt cctatcagta actgctccgt gttcagactc ctggtttctt 1920
ccaggcttac agtggacatc atcagcttcc tgctttaaaa aatatcttat gtcctaatt 1980
gcctttcttt tacctgactt tgtcaccttt gttgtctttg aattcttttag gctgcatatt 2040
attttacatg ctttgttttg tcatgtatat accaggattt ggttttatgg tttaaact 2100
atggatacag gggtttgttt tgcacaattt taatagtcac gcactacata atgatgtttt 2160
ggccaatgac agaccacgta tatgttggca gtctcataag attataatac tgtattttta 2220
ctataccttt tctgtgttta gatacaaata ccattatggt acagttgcct acagtattca 2280
gtgcagtaac atgatgtaca ggttttagtc ctgttttgca tttttcttag gttgtatgct 2340
cttctgtttt aaaggtttga atcaccagca tttttgtgat caaaatccta tttagaaaaa 2400
ataaaactac tttctgttta tctctttt 2427

```

<210> 22

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<223> chromosome 20 open reading frame 129 (C20orf129)
protein

<400> 22

```

Met Ala Arg Ala Cys Leu Ile Gln Arg Leu Pro Ile Lys Arg Asp Cys
 1             5             10             15

Thr Pro Val Phe Val Arg Gly Leu Ser Ser Pro Ser Ala Ala Met Ala
 20             25             30

Leu Leu Ser Glu Gly Leu Asp Glu Val Pro Ala Ala Cys Leu Ser Pro
 35             40             45

Cys Gly Pro Pro Asn Pro Thr Glu Leu Phe Ser Glu Ser Arg Arg Leu
 50             55             60

Ala Leu Glu Glu Leu Val Ala Gly Gly Pro Glu Ala Phe Ala Ala Phe
 65             70             75             80

Leu Arg Arg Glu Arg Leu Ala Arg Phe Leu Asn Pro Asp Glu Val His
 85             90             95

```

Ala Ile Leu Arg Ala Ala Glu Arg Pro Gly Glu Glu Gly Ala Ala Ala
100 105 110

Ala Ala Ala Ala Glu Asp Ser Phe Gly Ser Ser His Asp Cys Ser Ser
115 120 125

Gly Thr Tyr Phe Pro Glu Gln Ser Asp Leu Glu Pro Pro Leu Leu Glu
130 135 140

Leu Gly Trp Pro Ala Phe Tyr Gln Gly Ala Tyr Arg Gly Ala Thr Arg
145 150 155 160

Val Glu Thr His Phe Gln Pro Arg Gly Ala Gly Glu Gly Gly Pro Tyr
165 170 175

Gly Cys Lys Asp Ala Leu Arg Gln Gln Leu Arg Ser Ala Arg Glu Val
180 185 190

Ile Ala Val Val Met Asp Val Phe Thr Asp Ile Asp Ile Phe Arg Asp
195 200 205

Leu Gln Glu Ile Cys Arg Lys Gln Gly Val Ala Val Tyr Ile Leu Leu
210 215 220

Asp Gln Ala Leu Leu Ser Gln Phe Leu Asp Met Cys Met Asp Leu Lys
225 230 235 240

Val His Pro Glu Gln Glu Lys Leu Met Thr Val Arg Thr Ile Thr Gly
245 250 255

Asn Ile Tyr Tyr Ala Arg Ser Gly Thr Lys Ile Ile Gly Lys Val His
260 265 270

Glu Lys Phe Thr Leu Ile Asp Gly Ile Arg Val Ala Thr Gly Ser Tyr
275 280 285

Ser Phe Thr
290

<210> 23
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 52 (C20orf52)
protein

<400> 23
gacgcggggc cggaacgcga agaggggtggt ggagtcgggc taccactga ttttccttcc 60
cttacttccc ctgagccctt gggcccactt cccagcctac cgcttccgtc cccgcccagac 120
tcttgggcca gcgcctgggc ccacactttc ctatcccccg cagatgccgg tggcctggg 180
tccctacgga cagtcaccagc caagctgctt cgaccgtgtc aaaatgggct tcgtgatggg 240
ttgcgcggtg ggcattggcg ccggggcgct cttcggcacc ttttcctgtc tcaggatcgg 300
aatgcggggg cgagagctga tgggctggcat tgggaaaacc atgatgcaga gtggcggcac 360
ctttggcaca ttcattggcca ttgggatggg catccgatgc taacctatgt tgccaactac 420
atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagtaaaa 480
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aa 602

<210> 24
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chromosome 20 open reading frame 52 (C20orf52)
 protein

<400> 24
 Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe
 1 5 10 15
 Asp Arg Val Lys Met Gly Phe Val Met Gly Cys Ala Val Gly Met Ala
 20 25 30
 Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu Arg Ile Gly Met Arg
 35 40 45
 Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr Met Met Gln Ser Gly
 50 55 60
 Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
 65 70 75

<210> 25
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<220>
 <223> chromosome 20 open reading frame 20 (C20orf20)
 protein

<400> 25
 ctcccgccgg gggctccttg ctgggcccgg ccgcgggccat gggagaggcc gaggtgggcg 60
 gcggggggcg cgcaggcgac aagggcccgg gggaggcggc caccagcccg gcggaggaga 120
 cagtgggtgt gagccccgag gtggagggtgt gcctcttcca cgccatgctg ggccacaagc 180
 ccgtcggtgt gaaccgacac ttccacatga tttgtattcg ggacaagtgc agccagaaca 240
 tcgggcggca ggtcccatcc aaggtcatct gggaccatct gagcaccatg tacgacatgc 300
 aggcgctgca tgagtctgag attcttccat tccgaatcc agagaggaac ttcgtccttc 360
 cagaagagat cattcaggag gtccgagaag gaaaagtgat gatagaagag gagatgaaag 420
 aggagatgaa ggaagacgtg gacccccaca atggggctga cgatgttttt tcatcttcag 480
 ggagtttggg gaaagcatca gaaaaatcca gcaaagacaa agagaagaac tcctcagact 540
 tggggtgcaa agaaggcgca gacaagcgga agcgcgagcc ggtcaccgac aaagtcctga 600
 ccgcaaacag caacccttcc agtcccagtg ctgccaagcg gcgcccgcac tagaccctca 660
 gccctggtgg cggcagagaa gcgggcgagg cactgtggtc gctgaggggg ttggctgggt 720
 ctgagtgcc accccaggcc acagtgatac catcccagtg ccatgagccc acactgccc 780
 ccctcaggct ctccaggtgaa cgtggccgtc agcggggaaa cgtgtgtgtc agttggacca 840
 tgtgggaccc tgatggacct gaaagaccag gatcggtcca gctcagatat tgagggtctc 900
 gaagcctagt tctgtcttct ctggagcagc tgtggcttcc ccgtggctgc ttggtgacat 960
 ggattagcgc tacgtgggct gcagcatttg ggatccaggc tacctagagg ggcacgggc 1020
 cagggaaaac ctcgattag caagcaataa aaacatgacc tcaactcttc tcaaaggagc 1080
 ccctggtctt ccctgtgtga ctcaagttctt tccatctgtt tgtcccgtc caagcctctt 1140
 tctgcgctga ctgtgacatt ggaacgtggc ctctctgtca cccctccgt gccacgcat 1200
 gaaggccacc cccaccacc tgggaaacta agaactggat attttgcctc attcacttgt 1260
 actgtaacaa tgtatataat ttggttggtt tttcactatt taatttttaa gaagcctatt 1320
 ttactagtgt tttatatgaa caaagtactg cagaagttaa acctgtgttg tattttttct 1380
 gagatgtttt gctttaagag atactttttg ctcaagtttt atatgccaga tacagagaat 1440
 ttgtagcggg tatttttgta tgatctagta acttgcaaac agaccaaatg gatgagaggc 1500

```

ggggaccgtg cagctgtcgg ctgatgagga ggcgggccgcc ccagtgtga tggagatgcc 1560
actttcgtgt gactgcgaac attaaagcac aaaaaaaatc caaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680
aaaaaa                                           1685

```

```

<210> 26
<211> 204
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> chromosome 20 open reading frame 20 (C20orf20)
      protein

```

```

<400> 26
Met Gly Glu Ala Glu Val Gly Gly Gly Gly Ala Ala Gly Asp Lys Gly
  1              5              10              15

Pro Gly Glu Ala Ala Thr Ser Pro Ala Glu Glu Thr Val Val Trp Ser
      20              25              30

Pro Glu Val Glu Val Cys Leu Phe His Ala Met Leu Gly His Lys Pro
      35              40              45

Val Gly Val Asn Arg His Phe His Met Ile Cys Ile Arg Asp Lys Phe
      50              55              60

Ser Gln Asn Ile Gly Arg Gln Val Pro Ser Lys Val Ile Trp Asp His
      65              70              75              80

Leu Ser Thr Met Tyr Asp Met Gln Ala Leu His Glu Ser Glu Ile Leu
      85              90              95

Pro Phe Pro Asn Pro Glu Arg Asn Phe Val Leu Pro Glu Glu Ile Ile
      100             105             110

Gln Glu Val Arg Glu Gly Lys Val Met Ile Glu Glu Glu Met Lys Glu
      115             120             125

Glu Met Lys Glu Asp Val Asp Pro His Asn Gly Ala Asp Asp Val Phe
      130             135             140

Ser Ser Ser Gly Ser Leu Gly Lys Ala Ser Glu Lys Ser Ser Lys Asp
      145             150             155             160

Lys Glu Lys Asn Ser Ser Asp Leu Gly Cys Lys Glu Gly Ala Asp Lys
      165             170             175

Arg Lys Arg Ser Arg Val Thr Asp Lys Val Leu Thr Ala Asn Ser Asn
      180             185             190

Pro Ser Ser Pro Ser Ala Ala Lys Arg Arg Arg Thr
      195             200

```

```

<210> 27
<211> 3149
<212> DNA
<213> Homo sapiens

```

<220>

<223> chromosome 20 open reading frame 188 (C20orf188)
protein

<400> 27

gacatggcgg	cggcgccggt	agcgggctggg	tctggagccg	gccgagggag	acgggtcggca	60
gccacagtgg	cggcttgggg	cggatggggc	ggcgggccc	ggcctggtaa	cattctgctg	120
cagctgcggc	agggccagct	gaccggccgg	ggcctgggtc	ggcgggtgca	gttcactgag	180
acttttttga	cggagagggg	caaacaatcc	aagtggagtg	gaattcctca	gctgctcctc	240
aagctgcaca	ccaccagcca	cctccacagt	gactttgttg	agtgtcaaaa	catcctcaag	300
gaaatttctc	ctcttctctc	catggaggct	atggcatttg	ttactgaaga	gaggaaactt	360
acccaagaaa	ccacttatcc	aaatacttat	atttttgact	tgtttgagg	tggtgatctt	420
cttgtagaaa	ttcttatgag	gcctacgata	tctatccggg	gacagaaact	gaaaataagt	480
gatgaaatgt	ccaaggactg	cttgagtata	ctgtataata	cctgtgtctg	tacagagggg	540
gttacaaaag	gtttggcaga	aaagaatgac	tttgtgatct	tcctgtttac	attgatgaca	600
agtaagaaga	cattcttaca	aacagcaacc	ctcattgaag	atattttggg	tgtaaaaaag	660
gaaatgatcc	gactagatga	agtcaccaat	ctgagttcct	tagtatccaa	tttcgatcag	720
cagcagctcg	ctaatttctg	ccgatttctg	gctgtcacca	tttcagagat	ggatacaggg	780
aatgatgaca	agcacacgct	tcttgccaaa	aatgtctaac	agaagaagag	cttgagtttg	840
gggccttctg	cagctgaaat	caatcaagcg	gcccttctca	gcattcctgg	ctttgttgag	900
cggcttttgc	aactggcgac	tcgaaagggt	tcagagtcaa	cgggcacagc	cagcttctct	960
caggagttag	aagagtggta	cacatggcta	gacaatgctt	tggtgctaga	tgccctgatg	1020
cgagtggcca	atgaggagtc	agagcacaat	caagcctcca	tttgtgtccc	tcctccaggg	1080
gcttctgagg	agaatggcct	gcctcacacg	tcagccagaa	cccagctgcc	ccagtcaatg	1140
aagattatgc	atgagatcat	gtacaaactg	gaagtgtctt	atgtcctctg	cgtgctgctg	1200
atggggcgct	agcgaaccca	ggttcacaga	atgattgcag	agttcaagct	gatccctgga	1260
cttaataaatt	tgtttgacaa	actgatttgg	aggaagcatt	cagcatctgc	ccttgtcctc	1320
catggtcaca	accagaactg	tgactgtagc	ccggacatca	ccttgaagat	acagtttttg	1380
aggcttcttc	agagcttcag	tgaccaccac	gagaacaagt	acttgttact	caacaaccag	1440
gagctgaatg	aactcagtgc	catctctctc	aaggccaaca	tccttgaggt	ggaagctgtc	1500
ctcaacaccg	acaggagtct	gggtgtgtgat	gggaagaggg	gcttattaac	tcgtctgctg	1560
caggctcatga	agaaggagcc	agcagagtcg	tctttcaggt	tttggaagc	tcgggctgtg	1620
gagagtttcc	tcgaggggac	cacctcctat	gcagaccaga	tgttcctgct	gaagcgaggc	1680
ctcttgagc	acatccttta	ctgcattgtg	gacagcgagt	gtaagtcaag	ggatgtgctc	1740
cagagttact	ttgacctcct	gggggagctg	atgaagttca	acgttgatgc	attcaagaga	1800
ttcaataaat	atatcaacac	cgatgcaaag	ttccaggtat	tcctgaagca	gatcaacagc	1860
tccttggtgg	actccaacat	gctgggtgcg	tgtgtcactc	tgtccctgga	ccgatttgaa	1920
aaccaggtgg	atatgaaagt	tgccgaggta	ctgtctgaat	gccgcctgct	cgctacata	1980
tcacagtgct	ccacgcagat	gtccttctct	ttccgcctca	tcaacatcat	ccacgtgcag	2040
acgctgaccc	aggagaacgt	cagctgcctc	aacaccagcc	tggtgatcct	gatgtggccc	2100
cgacggaaa	agcggctgcc	cctgtacctg	cggctgctgc	agcggatgga	gcacagcaag	2160
aagtaccccg	gcttctgct	caacaacttc	cacaacctgc	tgcgcttctg	gcagcagcac	2220
tacctgcaca	aggacaagga	cagcacctgc	ctagagaaca	gctcctgcat	cagcttctca	2280
tactggaagg	agacagtgtc	catcctgttg	aaccgcggac	ggcagtcacc	ctctgctctc	2340
gttagctaca	ttgaggagcc	ctacatggac	atagacaggg	acttcactga	ggagtgcact	2400
tgggccaggc	ctcgggaggc	tgctgggcca	gtgtgggtga	gcgtgggtac	gatgccacac	2460
gccctgccct	gttcccgttc	ctccctgctg	ctctctgcct	gccccaggte	tttgggtaca	2520
ggcttggtgg	gagggaaagt	ctagaagccc	ttggtcccc	tggtgctgag	ggccctaggt	2580
catggagagc	ctcagtcctc	ataatgagga	cagggtagca	tgcccacctt	tccttcagaa	2640
ccctggggcc	cagggccacc	cagaggtaag	aggacattta	gcattagctc	tgtgtgagct	2700
cctgccggtt	tcttggtgtg	cagtcagtc	cagagtgggg	aggaagatat	gggtgacccc	2760
caccccccat	ctgtgagcca	agcctccctt	gtccctggcc	tttggaccca	ggcaaaggct	2820
tctgagccct	gggcaggggt	ggtgggtacc	agagaatgct	gccttcccc	aagcctgccc	2880
ctctgcctca	ttttcctgta	gtcctctctg	ttctgtttgc	tcattggctg	ctgtgttcac	2940
ccaagggggg	tctcccagaa	gtgagggggc	tttccctcca	tccttgagg	cacggggcag	3000
ctgtgcctgc	cctgcctctg	cctgaggcag	ccgctcctgc	ctgagcctgg	acatggggcc	3060
cttcttgttg	ttgcaattt	attaacagca	aataaaccaa	ttaaatggag	actattaaat	3120
aactttattt	taaaaaaaaa	aaaaaaaaaa				3149

<210> 28
 <211> 797
 <212> PRT
 <213> Homo sapiens

<220>
 <223> chromosome 20 open reading frame 188 (C20orf188)
 protein

<400> 28
 Met Ala Ala Ala Pro Val Ala Ala Gly Ser Gly Ala Gly Arg Gly Arg
 1 5 10 15
 Arg Ser Ala Ala Thr Val Ala Ala Trp Gly Gly Trp Gly Gly Arg Pro
 20 25 30
 Arg Pro Gly Asn Ile Leu Leu Gln Leu Arg Gln Gly Gln Leu Thr Gly
 35 40 45
 Arg Gly Leu Val Arg Ala Val Gln Phe Thr Glu Thr Phe Leu Thr Glu
 50 55 60
 Arg Asp Lys Gln Ser Lys Trp Ser Gly Ile Pro Gln Leu Leu Leu Lys
 65 70 75 80
 Leu His Thr Thr Ser His Leu His Ser Asp Phe Val Glu Cys Gln Asn
 85 90 95
 Ile Leu Lys Glu Ile Ser Pro Leu Leu Ser Met Glu Ala Met Ala Phe
 100 105 110
 Val Thr Glu Glu Arg Lys Leu Thr Gln Glu Thr Thr Tyr Pro Asn Thr
 115 120 125
 Tyr Ile Phe Asp Leu Phe Gly Gly Val Asp Leu Leu Val Glu Ile Leu
 130 135 140
 Met Arg Pro Thr Ile Ser Ile Arg Gly Gln Lys Leu Lys Ile Ser Asp
 145 150 155 160
 Glu Met Ser Lys Asp Cys Leu Ser Ile Leu Tyr Asn Thr Cys Val Cys
 165 170 175
 Thr Glu Gly Val Thr Lys Arg Leu Ala Glu Lys Asn Asp Phe Val Ile
 180 185 190
 Phe Leu Phe Thr Leu Met Thr Ser Lys Lys Thr Phe Leu Gln Thr Ala
 195 200 205
 Thr Leu Ile Glu Asp Ile Leu Gly Val Lys Lys Glu Met Ile Arg Leu
 210 215 220
 Asp Glu Val Pro Asn Leu Ser Ser Leu Val Ser Asn Phe Asp Gln Gln
 225 230 235 240
 Gln Leu Ala Asn Phe Cys Arg Ile Leu Ala Val Thr Ile Ser Glu Met
 245 250 255
 Asp Thr Gly Asn Asp Asp Lys His Thr Leu Leu Ala Lys Asn Ala Gln
 260 265 270

Gln Lys Lys Ser Leu Ser Leu Gly Pro Ser Ala Ala Glu Ile Asn Gln
 275 280 285
 Ala Ala Leu Leu Ser Ile Pro Gly Phe Val Glu Arg Leu Cys Lys Leu
 290 295 300
 Ala Thr Arg Lys Val Ser Glu Ser Thr Gly Thr Ala Ser Phe Leu Gln
 305 310 315 320
 Glu Leu Glu Glu Trp Tyr Thr Trp Leu Asp Asn Ala Leu Val Leu Asp
 325 330 335
 Ala Leu Met Arg Val Ala Asn Glu Glu Ser Glu His Asn Gln Ala Ser
 340 345 350
 Ile Val Phe Pro Pro Pro Gly Ala Ser Glu Glu Asn Gly Leu Pro His
 355 360 365
 Thr Ser Ala Arg Thr Gln Leu Pro Gln Ser Met Lys Ile Met His Glu
 370 375 380
 Ile Met Tyr Lys Leu Glu Val Leu Tyr Val Leu Cys Val Leu Leu Met
 385 390 395 400
 Gly Arg Gln Arg Asn Gln Val His Arg Met Ile Ala Glu Phe Lys Leu
 405 410 415
 Ile Pro Gly Leu Asn Asn Leu Phe Asp Lys Leu Ile Trp Arg Lys His
 420 425 430
 Ser Ala Ser Ala Leu Val Leu His Gly His Asn Gln Asn Cys Asp Cys
 435 440 445
 Ser Pro Asp Ile Thr Leu Lys Ile Gln Phe Leu Arg Leu Leu Gln Ser
 450 455 460
 Phe Ser Asp His His Glu Asn Lys Tyr Leu Leu Leu Asn Asn Gln Glu
 465 470 475 480
 Leu Asn Glu Leu Ser Ala Ile Ser Leu Lys Ala Asn Ile Pro Glu Val
 485 490 495
 Glu Ala Val Leu Asn Thr Asp Arg Ser Leu Val Cys Asp Gly Lys Arg
 500 505 510
 Gly Leu Leu Thr Arg Leu Leu Gln Val Met Lys Lys Glu Pro Ala Glu
 515 520 525
 Ser Ser Phe Arg Phe Trp Gln Ala Arg Ala Val Glu Ser Phe Leu Arg
 530 535 540
 Gly Thr Thr Ser Tyr Ala Asp Gln Met Phe Leu Leu Lys Arg Gly Leu
 545 550 555 560
 Leu Glu His Ile Leu Tyr Cys Ile Val Asp Ser Glu Cys Lys Ser Arg
 565 570 575
 Asp Val Leu Gln Ser Tyr Phe Asp Leu Leu Gly Glu Leu Met Lys Phe
 580 585 590

Asn	Val	Asp	Ala	Phe	Lys	Arg	Phe	Asn	Lys	Tyr	Ile	Asn	Thr	Asp	Ala	595	600	605
Lys	Phe	Gln	Val	Phe	Leu	Lys	Gln	Ile	Asn	Ser	Ser	Leu	Val	Asp	Ser	610	615	620
Asn	Met	Leu	Val	Arg	Cys	Val	Thr	Leu	Ser	Leu	Asp	Arg	Phe	Glu	Asn	625	630	635
Gln	Val	Asp	Met	Lys	Val	Ala	Glu	Val	Leu	Ser	Glu	Cys	Arg	Leu	Leu	645	650	655
Ala	Tyr	Ile	Ser	Gln	Val	Pro	Thr	Gln	Met	Ser	Phe	Leu	Phe	Arg	Leu	660	665	670
Ile	Asn	Ile	Ile	His	Val	Gln	Thr	Leu	Thr	Gln	Glu	Asn	Val	Ser	Cys	675	680	685
Leu	Asn	Thr	Ser	Leu	Val	Ile	Leu	Met	Leu	Ala	Arg	Arg	Lys	Glu	Arg	690	695	700
Leu	Pro	Leu	Tyr	Leu	Arg	Leu	Leu	Gln	Arg	Met	Glu	His	Ser	Lys	Lys	705	710	715
Tyr	Pro	Gly	Phe	Leu	Leu	Asn	Asn	Phe	His	Asn	Leu	Leu	Arg	Phe	Trp	725	730	735
Gln	Gln	His	Tyr	Leu	His	Lys	Asp	Lys	Asp	Ser	Thr	Cys	Leu	Glu	Asn	740	745	750
Ser	Ser	Cys	Ile	Ser	Phe	Ser	Tyr	Trp	Lys	Glu	Thr	Val	Ser	Ile	Leu	755	760	765
Leu	Asn	Pro	Asp	Arg	Gln	Ser	Pro	Ser	Ala	Leu	Val	Ser	Tyr	Ile	Glu	770	775	780
Glu	Pro	Tyr	Met	Asp	Ile	Asp	Arg	Asp	Phe	Thr	Glu	Glu				785	790	795